

SEQUENCE LISTING

<110> Garvan Institute of Medical Research

5 <120> Method of modulating bone growth, remodeling and adiposity

<130> 501789/MRO

<160> 20

10 <170> PatentIn version 3.1

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 Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly
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 Glu Thr Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr
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 Val Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu
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 55 atc atc aac cca aga ggg tgg aga cca aac aat aga cat gct tac ata 602
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 Gly Ile Thr Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe
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 55 gtg atc tat caa att ctg acc gac gag ccc ttc caa aat gtg tca ctt 698
 Val Ile Tyr Gln Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu
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 60 gcg gcg ttc aag gac aag tat gtg tgc ttt gac aaa ttc cca tct gac 746
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	Leu Lys Arg Arg Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr	
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	Arg Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val	
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	Val Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val	
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20	ttc gac tgg aac cac cag atc att gcc acc tgc aac cac aat ctg ctg	1034
	Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu	
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	ttt ctg ctc tgt cac ctc acc gcc atg atc tcc acc tgc gtc aac ccc	1082
	Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro	
	305 310 315	
25	atc ttt tat gga ttc ctg aac aaa aat ttc cag aga gac ttg cag ttc	1130
	Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe	
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30	ttc ttc aac ttt tgt gac ttc cgg tct cga gac gat gac tac gag acc	1178
	Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr	
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35	ata gcc atg tct acc atg cat acg gat gtg tcc aag acg tct ctg aag	1226
	Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys	
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40	cag gct agc cca gtc gca ttt aaa aaa atc agt atg aat gac aat gaa	1274
	Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu	
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 20 His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala
 35 40 45

 25 Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
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 30 Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
 65 70 75 80

 35 Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
 85 90 95

 40 Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
 100 105 110

 45 Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
 115 120 125

 50 Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
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 55 Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
 145 150 155 160

 60 Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln
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 65 Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys
 180 185 190

 70 Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
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 75 Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
 210 215 220

24

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 245 250 255
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 260 265 270
 15 Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn
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 20 His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys
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 His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
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 25 Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe
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 30 Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser
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10	aggatttgct tcatcaagct tttgcaagat ctacagtgtg atgaatcaga acacagctat	660
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	atg gtt ctg aag atg ggc ccg gta ggt gca gag gca gat gag aat caa	828
	Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln	
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	Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro	
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25	aga ggt gag ttg ccc cct gat ccg gag ccg gag ctc ata gac agc acc	924
	Arg Gly Glu Leu Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr	
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30	aaa ctg gtc gag gtg cag gtg atc ctc ata ttg gcc tac tgc tcc atc	972
	Lys Leu Val Glu Val Gln Val Ile Leu Ile Leu Ala Tyr Cys Ser Ile	
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	Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu	
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27

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 30 Arg Gly Glu Leu Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr
 35 40 45
 Lys Leu Val Glu Val Gln Val Ile Leu Ile Leu Ala Tyr Cys Ser Ile
 50 55 60
 35 Ile Leu Leu Gly Val Val Gly Asn Ser Leu Val Ile His Val Val Ile
 65 70 75 80
 40 Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu
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 45 Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu
 100 105 110
 50 Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His
 115 120 125
 Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr
 130 135 140
 55 Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu
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 60 Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala
 165 170 175
 Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu

28

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20	Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Arg Asn His Val Ser Pro 245 250 255		
25	Gly Ala Ala Ser Asp His Tyr His Gln Arg Arg His Lys Met Thr Lys 260 265 270		
30	Met Leu Val Cys Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu 275 280 285		
35	His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu 290 295 300		
40	Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys 305 310 315 320		
45	Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr 325 330 335		
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	gagttccatt tgtttgtttt gcaggtgca tctctgaagt aggccttta ctccgtgagt	180
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	ttc cca gga tcc cta cag ggt aag aat ggg acc aat cca ttg gat tcc	281
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	Pro Tyr Asn Phe Ser Asp Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala	
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	Phe Ile Ile Thr Thr Tyr Ser Ile Glu Thr Ile Leu Gly Val Leu Gly	
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25	aac ctc tgc ttg ata ttt gtg acc aca aga caa aag gaa aag tcc aat	425
	Asn Leu Cys Leu Ile Phe Val Thr Thr Arg Gln Lys Glu Lys Ser Asn	
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35	Cys Leu Ile Cys Gln Pro Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr	
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	Arg His Gln Leu Ile Ile Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe	
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5 ata cgc atc tac cag cgc ctg cag agg cag aag cat gtg ttc cat gcg 953
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10 cac gct tgc agc tca cga gcg ggg cag atg aag cgg atc aac agc atg 1001
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 255 260 265

15 ctc atg aca atg gtg act gcc ttt gca gtt ctc tgg cta ccc ctg cat 1049
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30 aag gat atc aag gct ctg gtg ctg acc tgc cat tgc agg tca cct caa 1241
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35 ggg gag tct gag cat ctg ccc ctg tcc act gtt cac acg gac ctc tcc 1289
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Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala Phe Ile Ile Thr Thr Tyr
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Ser Ile Glu Thr Ile Leu Gly Val Leu Gly Asn Leu Cys Leu Ile Phe
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Val Thr Thr Arg Gln Lys Glu Lys Ser Asn Val Thr Asn Leu Leu Ile
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Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Ile Cys Gln Pro
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Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Val
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Leu Cys Lys Met Leu Thr Phe Ile Gln Cys Met Ser Val Thr Val Ser
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Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile
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Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe Gln Ala Tyr Leu Gly Ile
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Val Val Ile Trp Phe Ile Ser Cys Phe Leu Ser Leu Pro Phe Leu Ala
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Asn Ser Thr Leu Asn Asp Leu Phe His Tyr Asn His Ser Lys Val Val
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Glu Phe Leu Glu Asp Lys Val Val Cys Phe Val Ser Trp Ser Ser Asp
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His His Arg Leu Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
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Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr Ile Arg Ile Tyr Gln Arg
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Leu Gln Arg Gln Lys His Val Phe His Ala His Ala Cys Ser Ser Arg
 245 250 255
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Ala Gly Gln Met Lys Arg Ile Asn Ser Met Leu Met Thr Met Val Thr
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Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Thr Leu Glu
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 20 Val Leu Thr Cys His Cys Arg Ser Pro Gln Gly Glu Ser Glu His Leu
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 60 Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe Pro Val Trp Glu Asp
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 Tyr Arg Gly Ser Val Asp Asn Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
 55 60 65
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2281

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